

re-run

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/798,602  
Source: 1FWO  
Date Processed by STIC: 3/22/04

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 05/25/2005

PATENT APPLICATION: US/10/798,602

TIME: 11:28:56

Input Set : N:\AMC\US10798602.raw

Output Set: N:\CRF4\05242005\J798602.raw

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1 <110> APPLICANT: Delcayre, Alain
2 <120> TITLE OF INVENTION: Compositions isolated from M. vaccae and
3   their use in modulation of immune responses.
4 <130> FILE REFERENCE: 11000.1047c2
5 <140> CURRENT APPLICATION NUMBER: US/10/798,602
6 <141> CURRENT FILING DATE: 2004-03-10
7 <150> PRIOR APPLICATION NUMBER: US 10/051,325
8 <151> PRIOR FILING DATE: 2002-01-18
9 <150> PRIOR APPLICATION NUMBER: US 09/455,960
10 <151> PRIOR FILING DATE: 1999-12-06
11 <160> NUMBER OF SEQ ID NOS: 31
12 <170> SOFTWARE: FastSEQ for Windows Version 3.0
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 402
16 <212> TYPE: DNA
17 <213> ORGANISM: Mycobacterium vaccae
18 <400> SEQUENCE: 1
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20   gacgtcatca tgctggatcg ttcggcgggg cacctgttcc agccgctgct ctatcagtgc      120
21   gcgacgggga cgctgagcat cgcgcacatc agtcgcccc tgcgcgagga gttcgcccgg      180
22   taccccaaca tcaggacgct gctcggcaag gcggtcgaga tcgaccccgga ccgccgggtg      240
23   gtgaccgcga tgagaccgga cgaatccacg ttcacgctcg actacgacgt gctcgtcgtc      300
24   gccgcccggc tgcagcagtc ctatttcggc aagcgtcatt tcgcgaggagtg ggcgccaggg      360
25   atgaagaccc tcgacgacgc gctgggcacg cggcagcgga tc                                402
27 <210> SEQ ID NO: 2
28 <211> LENGTH: 2500
29 <212> TYPE: DNA
30 <213> ORGANISM: Mycobacterium vaccae
31 <400> SEQUENCE: 2
32   gatcgccgcg cagtcggccg ccggcgccga gctggcctcc ggggtcggca ctctcgacga      60
33   tccgcgcgcc ggcgaggatc cgcaggccgc cgcactggcc gcatggtccc tggcgcacgg      120
34   cttcgcgatg ctgtggctca acaaggccgt cgccaccgac gccgaccggg tcgccaccgc      180
35   cgaaccgggt gcgcgcatgc tgttcacccc gaaccggccg gccgggaccc ccgacgagta      240
36   gcgtcggcgt catgactgac gctgcgatca ccgacatccc gctcaccacc ctggacggcc      300
37   ggcccaccac gctcgcggag ttggccgacg gcgcgcgct ggtggtcaat gtcgcctcca      360
38   aatgcggtct gacaccgcag tacacggcgc tcgaacagct cgcaaggac taccgtgaac      420
39   gcggactcac cgtgatcggc gtgccgtgca accagtccat ggggcaggag cccgggaccg      480
40   ccgaggagat ccagacgttc tgctcgacga cctacgacgt gacgttcccg ctgctggaga      540
41   agaccgacgt caacgggccc ggcaggcacc cgctctacgc cgagctggcc cgcgccaccg      600
42   acgaggacgg cgaggccggc gacgtgcagt ggaacttcga gaagtctctg ctgcgcccg      660
43   gcggcaaagt ggtcaggcgt ttccgtcccc gcaccgcccc ggacgcccc gaggtgatct      720
44   cggccatcga agacgtcttg ccccgatagc cgaagcgaca cctgggcgcg cgggtgctgc      780
45   cacctccagg acatatcgcg ttgcgacact tcggtggtgg caggacagct gatcgtgtcg      840

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46	atctccggaa	tcagtgaccg	gaccctcggt	gaggtcgccg	agttccggag	tgcgctcgac	900
47	gtccgtggcg	tgccggtgtc	gttcctcgtc	gcgcgcgctc	tcaagggcgg	gtaccggctg	960
48	gaccgggacg	cgccaccgt	cgactggctg	atcgaccggc	gccggcgccg	cgatgccgtc	1020
49	gtgctgcacg	gtttcgacga	ggcccggacc	acagcgccgc	gcggtgagtt	cgcgacgctg	1080
50	cccgcgcacg	aggcgaacct	gcgcctgatg	gccgcgcgac	ggatcatgga	gcacctggac	1140
51	ctgcgcaccc	ggatcttcgc	cgcgcgccgg	tggaaactct	ccccgggtgc	actcaaagta	1200
52	ctgccccgca	atgggtttcg	cgtccttgcc	gggtggcgcg	gcacgtcgca	cctggtcggt	1260
53	gggcacactg	tgcgcgcgct	ggtgctcggc	atcggcgggg	gcttcctcgc	cgaacctggg	1320
54	tggcgccgga	cgctggtgct	ggccgcgcaa	cgcacggcac	gccgcggcgg	aacctgcccg	1380
55	ctgacggtgt	cgcccgccga	gctgagccgc	ccgggtcccc	ggcaaacctc	gctcgacgcc	1440
56	gtcgaactgg	cgatgctgca	ctcgggcgcg	gccacggtct	accggtggca	ccccgaatct	1500
57	gcgctgaccg	aggccgctta	gcggccctcg	ctgactacat	tggcctgatg	gctgatgtca	1560
58	tcgttggtgg	gcgcggggct	ggctggtctg	gtcgcagcgt	gcgagctggc	cgagcgccgc	1620
59	cgaagcgtgg	ttgactacat	tggcctgatg	gctgatgtca	tcgttggtgg	gcgcggggct	1680
60	ggctggtctg	gtcgcagcgt	gcgagctggc	cgagcgccgc	cgaagcgtgg	tgatcgtcga	1740
61	ccaggagaac	gcggccaatg	tcggcgccca	ggcgttctgg	tcgttcggcg	ggctgttctt	1800
62	cgtcgacagc	ccggagcagc	ggcgcatggg	catccgggac	agtcacgagc	tcgcgctgca	1860
63	ggactggctc	ggctcggccg	ggttcgaccg	gcccgaggac	cactggccgc	ggctgtgggc	1920
64	ccacgcctac	gtcgacttcg	ccgcggcgga	gaagcgcagc	tggctgcgcg	agcgcggtct	1980
65	gcagaccttc	gcgctggtcg	gctggggccga	acgcggcgcc	tacggggcca	acgggcacgg	2040
66	caactcggtg	ccgcgcttcc	acatcacgtg	gggcaccggg	cccgcgctgg	tcgacatctt	2100
67	cgcgcggcgg	ttgaccgggg	tgcgcggggt	gcggttcgct	caccggcacc	gggtggacga	2160
68	gctgatcgtc	gaggacgggt	cgggtggtcg	ggtgcgcgga	gccgtactgg	aaccgtcgtc	2220
69	ggcgggtacc	ggtgcggaat	cctcccgcga	ggtcgtcgcc	gacttcgaga	tgcgggcgca	2280
70	ggcggtgac	gtggccagcg	gcgggacgcg	gggcaaccac	gacctggtgc	gcaaatactg	2340
71	gcccgaagcg	atgggacggg	tgcccgaaca	actgctcagc	ggtgtgcccg	cgcacgtcga	2400
72	cggacgcgat	ctgcagatct	cggagaccgc	gggtgccagc	gtcatcaaca	aagaccggat	2460
73	gtggcaactac	accgagggca	tcaccaacta	cgacccgatc			2500

75 &lt;210&gt; SEQ ID NO: 3

76 &lt;211&gt; LENGTH: 498

77 &lt;212&gt; TYPE: DNA

78 &lt;213&gt; ORGANISM: Mycobacterium vaccae

79 &lt;400&gt; SEQUENCE: 3

80	atgactgacg	ctgcgatcac	cgacatcccg	ctcaccaccc	tggacggccg	gccaccacg	60
81	ctcgcggagt	tggccgacgg	cgcgcgcgtg	gtggtcaatg	tcgcctccaa	atgcggctctg	120
82	acaccgcagt	acacggcgct	cgaacagctc	gcgaaggact	accgtgaacg	cggactcacc	180
83	gtgatcggcg	tgccgtgcaa	ccagttcatg	gggcaggagc	ccgggaccgc	cgaggagatc	240
84	cagacgttct	gctcgacgac	ctacgacgtg	acgttcccgc	tgctggagaa	gaccgacgtc	300
85	aacggggccc	gcaggcatcc	gctctacgcc	gagctggccc	gcgccaccga	cgaggacggc	360
86	gaggccggcg	acgtgcagtg	gaacttcgag	aagttcctgc	tcgccccggg	cggcaaagtg	420
87	gtcaggcggt	tccgtccccg	caccgccccg	gacgcccccg	aggatgatctc	ggccatcgaa	480
88	gacgtcttgc	cccgatag					498

90 &lt;210&gt; SEQ ID NO: 4

91 &lt;211&gt; LENGTH: 687

92 &lt;212&gt; TYPE: DNA

93 &lt;213&gt; ORGANISM: Mycobacterium vaccae

94 &lt;400&gt; SEQUENCE: 4

95	gtgtcgatct	ccggaatcag	tgaccggacc	ctcggtgagg	tcgccgagtt	ccggagtgcg	60
96	ctcgacgtcc	gtggcggtgc	ggtgtcgttc	ctcgtcgcgc	cgcgtctcaa	gggcgggtac	120

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97      cggctggacc gggacgcggc caccgtcgac tggctgatcg accggcgccg gcgcggcgat      180
98      gccgtcgtgc tgcacggttt cgacgaggcc cggaccacag cgcgccgcgg tgagttcgcg      240
99      acgtgcccg cgcacgaggc gaacctgcgc ctgatggccg ccgacaggat catggagcac      300
100     ctggacctgc gcacccggat cttcgcgcgc cccggctgga acgtctcccc ggggtgactc      360
101     aaagtactgc cccgcaatgg gtttcgcgtc cttgccgggc tggcgggcat cgtcgacctg      420
102     gtcggtgggc aactgtgcgc cgcgcgggtg ctcggcatcg gcgggggctt cctcgccgaa      480
103     ccgtggtggt gccggacgct ggtgctggcc gccgaacgca cggcacgccg cggcggaacc      540
104     gtgcggctga cgggtgtcggc ccggcagctg agccgcccgg gtccccggca aacctgtctc      600
105     gacgccgtcg aactggcgat gctgcactcg ggcgcggcca cgggtctaccg gtggcacccc      660
106     gaatctgcgc tgaccgaggc cgcttag      687
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109 <211> LENGTH: 846
110 <212> TYPE: DNA
111 <213> ORGANISM: Mycobacterium vaccae
112 <400> SEQUENCE: 5
113     atgtcatcgt tgggtgggcgc cgggctggct ggtctggctg cagcgtgcga gctggccgag      60
114     cgcggccgaa gcgtggtgat cgtcgaccag gagaacgcgg ccaatgtcgg cggccaggcg      120
115     ttctggctgt tcggcgggct gttcttcgtc gacagcccgg agcagcggcg catgggcatc      180
116     cgggacagtc acgagctcgc gctgcaggac tggctcggct cggccggggt cgaccggccc      240
117     gaggaccact ggccgcggct gtgggcccac gcctacgtcg acttcgcgc cggcgagaag      300
118     cgcagctggc tgcgcgagcg cgggtctgcag accttcgcgc tggctcggctg ggccgaacgc      360
119     ggcggttacg gggccaacgc gcacggcaac tcggtgccgc gttccacat cactgggggc      420
120     accgggcccg cgtggttcga catcttcgcg cggcggttga ccggggtgcc gcgggtgcgg      480
121     ttctccacc ggcaccgggt ggacgagctg atcgtcgagg acggtgcggt ggtcgggggtg      540
122     cgcggagccg tactggaacc gtcgtcggcg gtaccgggtg cggaatcctc ccgcgaggtc      600
123     gtcggcgact tcgagatgcg ggcgcaggcg gtgatcgtgg ccagcggcgg gatcgggggc      660
124     aaccacgacc tgggtgcgaa atactggccc aagcggatgg gacgggtgcc cgaacaactg      720
125     ctacgcggtg tgcccgcgca cgtcgacgga cgcgtgctgc agatctcgga gaccgcgggt      780
126     gccagcgtca tcaacaaaga ccggatgtgg cactacaccg agggcatcac caactacgac      840
127     ccgac      846
129 <210> SEQ ID NO: 6
130 <211> LENGTH: 134
131 <212> TYPE: PRT
132 <213> ORGANISM: Mycobacterium vaccae
133 <400> SEQUENCE: 6
134     Ile Ile Gly Gly Phe Gly Gly Leu Phe Cys Ala Arg Arg Leu Ala
135     1           5           10           15
136     Arg Ser Ala Val Asp Val Ile Met Leu Asp Arg Ser Ala Gly His Leu
137     20           25           30
138     Phe Gln Pro Leu Leu Tyr Gln Cys Ala Thr Gly Thr Leu Ser Ile Ala
139     35           40           45
140     His Ile Ser Arg Pro Leu Arg Glu Glu Phe Ala Arg Tyr Pro Asn Ile
141     50           55           60
142     Arg Thr Leu Leu Gly Lys Ala Val Glu Ile Asp Pro Asp Arg Arg Val
143     65           70           75           80
144     Val Thr Ala Met Arg Pro Asp Glu Ser Thr Phe Thr Leu Asp Tyr Asp
145     85           90           95
146     Val Leu Val Val Ala Ala Gly Met Gln Gln Ser Tyr Phe Gly Lys Arg
147     100          105          110

```

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148      His Phe Ala Glu Trp Ala Pro Gly Met Lys Thr Leu Asp Asp Ala Leu
149              115                      120                      125
150      Gly Ile Arg Gln Arg Ile
151              130
153 <210> SEQ ID NO: 7
154 <211> LENGTH: 165
155 <212> TYPE: PRT
156 <213> ORGANISM: Mycobacterium vaccae
157 <400> SEQUENCE: 7
158      Met Thr Asp Ala Ala Ile Thr Asp Ile Pro Leu Thr Thr Leu Asp Gly
159              1              5              10              15
160      Arg Pro Thr Thr Leu Ala Glu Leu Ala Asp Gly Ala Ala Leu Val Val
161              20              25              30
162      Asn Val Ala Ser Lys Cys Gly Leu Thr Pro Gln Tyr Thr Ala Leu Glu
163              35              40              45
164      Gln Leu Ala Lys Asp Tyr Arg Glu Arg Gly Leu Thr Val Ile Gly Val
165              50              55              60
166      Pro Cys Asn Gln Phe Met Gly Gln Glu Pro Gly Thr Ala Glu Glu Ile
167              65              70              75              80
168      Gln Thr Phe Cys Ser Thr Thr Tyr Asp Val Thr Phe Pro Leu Leu Glu
169              85              90              95
170      Lys Thr Asp Val Asn Gly Pro Gly Arg His Pro Leu Tyr Ala Glu Leu
171              100             105             110
172      Ala Arg Ala Thr Asp Glu Asp Gly Glu Ala Gly Asp Val Gln Trp Asn
173              115             120             125
174      Phe Glu Lys Phe Leu Leu Ala Pro Gly Gly Lys Val Val Arg Arg Phe
175              130             135             140
176      Arg Pro Arg Thr Ala Pro Asp Ala Pro Glu Val Ile Ser Ala Ile Glu
177              145             150             155             160
178      Asp Val Leu Pro Arg
179              165
181 <210> SEQ ID NO: 8
182 <211> LENGTH: 228
183 <212> TYPE: PRT
184 <213> ORGANISM: Mycobacterium vaccae
185 <400> SEQUENCE: 8
186      Val Ser Ile Ser Gly Ile Ser Asp Arg Thr Leu Gly Glu Val Ala Glu
187              1              5              10              15
188      Phe Arg Ser Ala Leu Asp Val Arg Gly Val Pro Val Ser Phe Leu Val
189              20              25              30
190      Ala Pro Arg Leu Lys Gly Gly Tyr Arg Leu Asp Arg Asp Ala Ala Thr
191              35              40              45
192      Val Asp Trp Leu Ile Asp Arg Arg Arg Arg Gly Asp Ala Val Val Leu
193              50              55              60
194      His Gly Phe Asp Glu Ala Arg Thr Thr Ala Arg Arg Gly Glu Phe Ala
195              65              70              75              80
196      Thr Leu Pro Ala His Glu Ala Asn Leu Arg Leu Met Ala Ala Asp Arg
197              85              90              95
198      Ile Met Glu His Leu Asp Leu Arg Thr Arg Ile Phe Ala Ala Pro Gly

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199          100          105          110
200  Trp Asn Val Ser Pro Gly Ala Leu Lys Val Leu Pro Arg Asn Gly Phe
201          115          120          125
202  Arg Val Leu Ala Gly Leu Ala Gly Ile Val Asp Leu Val Gly Gly His
203          130          135          140
204  Thr Val Arg Ala Arg Val Leu Gly Ile Gly Gly Phe Leu Ala Glu
205          145          150          155          160
206  Pro Trp Trp Cys Arg Thr Leu Val Leu Ala Ala Glu Arg Thr Ala Arg
207          165          170          175
208  Arg Gly Gly Thr Val Arg Leu Thr Val Ser Ala Arg Gln Leu Ser Arg
209          180          185          190
210  Pro Gly Pro Arg Gln Thr Leu Leu Asp Ala Val Glu Leu Ala Met Leu
211          195          200          205
212  His Ser Gly Ala Ala Thr Val Tyr Arg Trp His Pro Glu Ser Ala Leu
213          210          215          220
214  Thr Glu Ala Ala
215          225
217 <210> SEQ ID NO: 9
218 <211> LENGTH: 282
219 <212> TYPE: PRT
220 <213> ORGANISM: Mycobacterium vaccae
221 <400> SEQUENCE: 9
222  Met Ser Ser Leu Val Gly Ala Gly Leu Ala Gly Leu Val Ala Ala Cys
223    1          5          10          15
224  Glu Leu Ala Glu Arg Gly Arg Ser Val Val Ile Val Asp Gln Glu Asn
225          20          25          30
226  Ala Ala Asn Val Gly Gly Gln Ala Phe Trp Ser Phe Gly Gly Leu Phe
227          35          40          45
228  Phe Val Asp Ser Pro Glu Gln Arg Arg Met Gly Ile Arg Asp Ser His
229          50          55          60
230  Glu Leu Ala Leu Gln Asp Trp Leu Gly Ser Ala Gly Phe Asp Arg Pro
231          65          70          75          80
232  Glu Asp His Trp Pro Arg Leu Trp Ala His Ala Tyr Val Asp Phe Ala
233          85          90          95
234  Ala Gly Glu Lys Arg Ser Trp Leu Arg Glu Arg Gly Leu Gln Thr Phe
235          100          105          110
236  Ala Leu Val Gly Trp Ala Glu Arg Gly Gly Tyr Gly Ala Asn Gly His
237          115          120          125
238  Gly Asn Ser Val Pro Arg Phe His Ile Thr Trp Gly Thr Gly Pro Ala
239          130          135          140
240  Leu Val Asp Ile Phe Ala Arg Arg Leu Thr Gly Val Pro Arg Val Arg
241          145          150          155          160
242  Phe Val His Arg His Arg Val Asp Glu Leu Ile Val Glu Asp Gly Ala
243          165          170          175
244  Val Val Gly Val Arg Gly Ala Val Leu Glu Pro Ser Ser Ala Val Pro
245          180          185          190
246  Gly Ala Glu Ser Ser Arg Glu Val Val Gly Asp Phe Glu Met Arg Ala
247          195          200          205
248  Gln Ala Val Ile Val Ala Ser Gly Gly Ile Gly Gly Asn His Asp Leu

```

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 19,20,21,22,23,24,25  
Seq#:2; Line(s) 32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51  
Seq#:2; Line(s) 52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71  
Seq#:2; Line(s) 72,73  
Seq#:3; Line(s) 80,81,82,83,84,85,86,87,88  
Seq#:4; Line(s) 95,96,97,98,99,100,101,102,103,104,105,106  
Seq#:5; Line(s) 113,114,115,116,117,118,119,120,121,122,123,124,125,126,127  
Seq#:10; Line(s) 264,265,266,267,268  
Seq#:11; Line(s) 275  
Seq#:12; Line(s) 282  
Seq#:13; Line(s) 289  
Seq#:14; Line(s) 296  
Seq#:15; Line(s) 303  
Seq#:16; Line(s) 310  
Seq#:17; Line(s) 317  
Seq#:18; Line(s) 324  
Seq#:19; Line(s) 331  
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Seq#:21; Line(s) 345  
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Seq#:25; Line(s) 373  
Seq#:26; Line(s) 380  
Seq#:27; Line(s) 387  
Seq#:28; Line(s) 394  
Seq#:29; Line(s) 401  
Seq#:30; Line(s) 408

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